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TECH CENTER 1600129001

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/486,882

DATE: 08/15/2001
TIME: 09:29:27

Input Set : A:\Try22410.app
Output Set: N:\CRF3\08132001\I486882.raw

3 <110> APPLICANT: Rowett Research Institute Services limited
5 <120> TITLE OF INVENTION: Chimeric binding peptide library screening method
7 <130> FILE REFERENCE: P22410-/scr/bou
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/486,882
C--> 10 <141> CURRENT FILING DATE: 2000-03-02
12 <160> NUMBER OF SEQ ID NOS: 78
14 <170> SOFTWARE: PatentIn Ver. 2.0
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 521
18 <212> TYPE: DNA
19 <213> ORGANISM: Recombinant human oestrogen
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (41)..(475)
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28 1 5
30 cct acg gca gcc gct gga ttg tta tta ctc gcg gcc cag ccg gcc atg 103
31 Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala Ala Gln Pro Ala Met
32 10 15 20
34 gcc caa gtg cag ctg cag taa tag gcg gcc gca ggg gga gga ggg tcc 151
35 Ala Gln Val Gln Leu Gln Ala Ala Ala Gly Gly Gly Gly Ser
W--> 36 25 30 35
38 atg gaa tct gcc aag gag act cgc tac tgt gca gtg tgc aat gac tat 199
39 Met Glu Ser Ala Lys Glu Thr Arg Tyr Cys Ala Val Cys Asn Asp Tyr
W--> 40 40 45 50
42 gct tca ggc tac cat tat gga gtc tgg tcc tgt gag ggc tgc aag gcc 247
43 Ala Ser Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala
W--> 44 55 60 65
46 ttc ttc aag aga agt att caa gga cat aac gac tat atg tgt cca gcc 295
47 Phe Phe Lys Arg Ser Ile Gln Gly His Asn Asp Tyr Met Cys Pro Ala
W--> 48 70 75 80 85
50 acc aac cag tgc acc att gat aaa aac agg agg aag agc tgc cag gcc 343
51 Thr Asn Gln Cys Thr Ile Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala
W--> 52 90 95 100
54 tgc cgg ctc cgt aaa tgc tac gaa gtg gga atg atg aaa ggt ggg ata 391
55 Cys Arg Leu Arg Lys Cys Tyr Glu Val Gly Met Met Lys Gly Gly Ile
W--> 56 105 110 115
58 cga aaa gac cga aga gga ggg aga atg ttg aaa cac aag cgc cag aga 439
59 Arg Lys Asp Arg Arg Gly Gly Arg Met Leu Lys His Lys Arg Gln Arg
W--> 60 120 125 130
62 gat gat ggg gag ggc agg ggt gaa gtg ggg tct tga taatcaggtc 485
63 Asp Asp Gly Glu Gly Arg Gly Glu Val Gly Ser
W--> 64 135 140 145
66 agagtgcct gagctaaaat aacacattca gaattc 521
69 <210> SEQ ID NO: 2

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p.5

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70 <211> LENGTH: 27
71 <212> TYPE: PRT
72 <213> ORGANISM: Recombinant human oestrogen
74 <400> SEQUENCE: 2
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78 Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln
79           20           25
82 <210> SEQ ID NO: 3
83 <211> LENGTH: 115
84 <212> TYPE: PRT
85 <213> ORGANISM: Recombinant human oestrogen
87 <400> SEQUENCE: 3
88 Ala Ala Ala Gly Gly Gly Gly Ser Met Glu Ser Ala Lys Glu Thr Arg
89   1           5           10           15
91 Tyr Cys Ala Val Cys Asn Asp Tyr Ala Ser Gly Tyr His Tyr Gly Val
92           20           25           30
94 Trp Ser Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser Ile Gln Gly
95           35           40           45
97 His Asn Asp Tyr Met Cys Pro Ala Thr Asn Gln Cys Thr Ile Asp Lys
98           50           55           60
100 Asn Arg Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys Cys Tyr Glu
101   65           70           75           80
103 Val Gly Met Met Lys Gly Gly Ile Arg Lys Asp Arg Arg Gly Gly Arg
104           85           90           95
106 Met Leu Lys His Lys Arg Gln Arg Asp Gly Glu Gly Arg Gly Glu
107           100          105          110
109 Val Gly Ser
110           115
113 <210> SEQ ID NO: 4
114 <211> LENGTH: 102
115 <212> TYPE: DNA
116 <213> ORGANISM: human
118 <220> FEATURE:
119 <221> NAME/KEY: CDS
120 <222> LOCATION: (1)..(102)
122 <400> SEQUENCE: 4
123 aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat      48
124 Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
125   1           5           10           15
127 gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac      96
128 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
129           20           25           30
131 ttc tat                                                                102
132 Phe Tyr
135 <210> SEQ ID NO: 5
136 <211> LENGTH: 34
137 <212> TYPE: PRT
138 <213> ORGANISM: human

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140 <400> SEQUENCE: 5

141 Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp

142 1 5 10 15

144 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn

145 20 25 30

147 Phe Tyr

151 <210> SEQ ID NO: 6

152 <211> LENGTH: 150

153 <212> TYPE: DNA

154 <213> ORGANISM: Human lymphocyte

156 <220> FEATURE:

157 <221> NAME/KEY: CDS

158 <222> LOCATION: (1)..(150)

160 <220> FEATURE:

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165 1 5 10 15

167 aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat 96

168 Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp

169 20 25 30

171 gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac 144

172 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn

173 35 40 45

175 ttc tat 150

176 Phe Tyr

177 50

180 <210> SEQ ID NO: 7

181 <211> LENGTH: 50

182 <212> TYPE: PRT

183 <213> ORGANISM: Human lymphocyte

185 <400> SEQUENCE: 7

186 Met Ala Gln Pro Thr Thr Arg Pro Gly Gln Gly Thr Arg Leu Asp Ile

187 1 5 10 15

189 Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp

190 20 25 30

192 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn

193 35 40 45

195 Phe Tyr

196 50

199 <210> SEQ ID NO: 8

200 <211> LENGTH: 150

201 <212> TYPE: DNA

202 <213> ORGANISM: Human lymphocyte

204 <220> FEATURE:

205 <221> NAME/KEY: CDS

206 <222> LOCATION: (1)..(150)

208 <400> SEQUENCE: 8

209 atg gcc cag tcc cac cac gcg tcc ggc gga ggg acc aag gtg gag atc 48

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210 Met Ala Gln Ser His His Ala Ser Gly Gly Gly Thr Lys Val Glu Ile
211   1           5           10           15
213 aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat   96
214 Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
215           20           25           30
217 gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac   144
218 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
219           35           40           45
221 ttc tat   150
222 Phe Tyr
223   50
226 <210> SEQ ID NO: 9
227 <211> LENGTH: 50
228 <212> TYPE: PRT
229 <213> ORGANISM: Human lymphocyte
231 <400> SEQUENCE: 9
232 Met Ala Gln Ser His His Ala Ser Gly Gly Gly Thr Lys Val Glu Ile
233   1           5           10           15
235 Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
236           20           25           30
238 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
239           35           40           45
241 Phe Tyr
242   50
245 <210> SEQ ID NO: 10
246 <211> LENGTH: 566
247 <212> TYPE: DNA
248 <213> ORGANISM: Recombinant human oestrogen
250 <220> FEATURE:
251 <221> NAME/KEY: CDS
252 <222> LOCATION: (41)..(475)
254 <400> SEQUENCE: 10
255 aagcttgcat gcaaattcta tttcaaggag acagtcataa atg aaa tac cta ttg   55
256                               Met Lys Tyr Leu Leu
257                               1           5
259 cct acg gca gcc gct gga ttg tta tta ctc gcg gcc cag ccg gcc atg   103
260 Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala Ala Gln Pro Ala Met
261           10           15           20
263 gcc gag gtg caa ctg cag taa tag gcg gcc gca ggg gga gga ggg tcc   151
264 Ala Glu Val Gln Leu Gln Ala Ala Ala Gly Gly Gly Gly Ser
W--> 265           25           30           35
267 atg gaa tct gcc aag gag act cgc tac tgt gca gtg tgc aat gac tat   199
268 Met Glu Ser Ala Lys Glu Thr Arg Tyr Cys Ala Val Cys Asn Asp Tyr
W--> 269           40           45           50
271 gct tca ggc tac cat tat gga gtc tgg tcc tgt gag ggc tgc aag gcc   247
272 Ala Ser Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala
W--> 273           55           60           65
275 ttc ttc aag aga agt att caa gga cat aac gac tat atg tgt cca gcc   295
276 Phe Phe Lys Arg Ser Ile Gln Gly His Asn Asp Tyr Met Cys Pro Ala

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W--> 277 70 75 80 85
279 acc aac cag tgc acc att gat aaa aac agg agg aag agc tgc cag gcc 343
280 Thr Asn Gln Cys Thr Ile Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala
W--> 281 90 95 100
283 tgc cgg ctc cgt aaa tgc tac gaa gtg gga atg atg aaa ggt ggg ata 391
284 Cys Arg Leu Arg Lys Cys Tyr Glu Val Gly Met Met Lys Gly Gly Ile
W--> 285 105 110 115
287 cga aaa gac cga aga gga ggg aga atg ttg aaa cac aag cgc cag aga 439
288 Arg Lys Asp Arg Arg Gly Gly Arg Met Leu Lys His Lys Arg Gln Arg
W--> 289 120 125 130
291 gat gat ggg gag ggc agg ggt gaa gtg ggg tct tga taatcaggtc 485
292 Asp Asp Gly Glu Gly Arg Gly Glu Val Gly Ser
W--> 293 135 140 145
295 agagtgcact gagctaaaat aacacattca ggctcgacttg ggtcagtctg accgggacaa 545
297 agttaatgta acctcgaatt c 566
300 <210> SEQ ID NO: 11
301 <211> LENGTH: 27
302 <212> TYPE: PRT
303 <213> ORGANISM: Recombinant human oestrogen
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307 1 5 10 15
309 Ala Gln Pro Ala Met Ala Glu Val Gln Leu Gln
310 20 25
313 <210> SEQ ID NO: 12
314 <211> LENGTH: 115
315 <212> TYPE: PRT
316 <213> ORGANISM: Recombinant human oestrogen
318 <400> SEQUENCE: 12
319 Ala Ala Ala Gly Gly Gly Gly Ser Met Glu Ser Ala Lys Glu Thr Arg
320 1 5 10 15
322 Tyr Cys Ala Val Cys Asn Asp Tyr Ala Ser Gly Tyr His Tyr Gly Val
323 20 25 30
325 Trp Ser Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser Ile Gln Gly
326 35 40 45
328 His Asn Asp Tyr Met Cys Pro Ala Thr Asn Gln Cys Thr Ile Asp Lys
329 50 55 60
331 Asn Arg Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys Cys Tyr Glu
332 65 70 75 80
334 Val Gly Met Met Lys Gly Gly Ile Arg Lys Asp Arg Arg Gly Gly Arg
335 85 90 95
337 Met Leu Lys His Lys Arg Gln Arg Asp Gly Glu Gly Arg Gly Glu
338 100 105 110
340 Val Gly Ser
341 115
344 <210> SEQ ID NO: 13
345 <211> LENGTH: 539
346 <212> TYPE: DNA
347 <213> ORGANISM: Recombinant human oestrogen

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY. *

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Output Set: N:\CRF3\08132001\I486882.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:36 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:40 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:44 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:48 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:52 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:56 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:60 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:64 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:265 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:269 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:273 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:277 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:281 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:285 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:289 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:293 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:612 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:21
L:612 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21
L:612 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21